

Docket No: 04983.0207.00US00/38-10(15498)A
Application Serial No. 09/404,520

REMARKS

In view of applicants' prior non-compliant amendment filed on 3/30/01 in response to the requirement for restriction and election, please cancel claims 1-28 and 31-46 without prejudice. The elected group XI claims, i.e. original claims 29 and 30, are believed to be patentable but are amended to more particularly point out and distinctly claim the full scope and breadth of the invention. Added are new claims 47-58 which are dependent from claim 29 and are supported by specification as filed. For instance, the subsets of recorded sequence in new claims 47-54 are found in the subsets of original claims 2-8; the homology searching limitations in new claims 55-56 are found in the specification at pages 37-39; computer based systems of new claim 57 is found at pages 38-39 and methods of identifying nucleotide sequence using the medium in new claim 58 is found at page 38.

Applicants continue to traverse the requirement to elect a single nucleic acid sequence. Independent claim 29 is directed to "computer readable medium having recorded thereon *at least 100* of the nucleotide sequences depicted in SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof." A restriction to a single nucleotide sequence prevents the claimed invention of *at least 100* sequences from ever being examined.

Although applicants believe that the claimed invention should be examined without a sequence restriction, applicants provisionally elect a 100 nucleotide sequence set (SEQ ID NO: 16207 through 16306) and a single sequence (SEQ ID NO: 16207).

Because the restriction to a single nucleotide sequence prevents the examination of applicants' claimed invention, the undersigned respectfully requests an interview to discuss the single sequence restriction.

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Marked-Up Version of Amended Claims

29. (Amended) Computer readable medium having recorded thereon at least 100 of the nucleotide sequences [depicted in] selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 [or] and complements thereof.
30. (Amended) Computer readable medium according to claim 29, having recorded thereon at least 1000 of said nucleotide sequences.
47. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 26804 and complements thereof.
48. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 25999 and complements thereof.
49. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 24034 and complements thereof.
50. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 22709 and complements thereof.
51. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17680 and complements thereof.
52. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17617 complements thereof.

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53. (New) Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17294 and complements thereof.
54. (New) Computer readable medium comprising the nucleotide sequences of the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 26804.
55. (New) Computer readable medium of claim 29 which is adapted for homology searching of nucleotide sequence.
56. (New) Computer readable medium of claim 55 wherein said medium is adapted for homology searching using a BLAST algorithm.
57. (New) A computer based system comprising computer readable medium of claim 29, input means for receiving a target sequence, means for identifying fragments of sequence recorded in said computer readable medium which are homologous to a target sequence, and an output means for outputting identified homologous sequences.
58. (New) A method of identifying nucleotide sequence comprising comparing target sequence to a sequence stored in computer readable medium of claim 29.

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